

A

Oilgo #	Name	Primer Sequences (5'-3')
2663	mK1	TTG GTG CTG ATG TTC TGG
2664	mK2	ATC TTC TTG CTG TTC TGG
2665	mK3	TGG GTG CTG CTG CTC TGG
2666	mK4	GGG CTG CTT GTG CTC TGG
2667	mK5	GGA ATC TTG TTG CTC TGG
2668	mK6	RTR TTS CTG CTG CTR TGG
2669	mK7	GGT CTC CTG TTG CTC TGT
2670	mK8	ATA TTT CTA CTG CTC TGT
2671	mK9	GTC ATA ATR TCC AGA GGA

B

Oilgo #	Name	Primer Sequences (5'-3')
2672	mH1	CTG AGC TGT GTA TTC CT
2673	mH2	CTC ARM TTG ATT TTC CT
2674	mH3	TGG RTC ATS TTC TTC CT
2675	mH4	TKS RTC TTT CTC TTC CT
2676	mH5	TGT ATC ATS CTC TTC TT
2677	mH6	TGG RTC TTT CTC TTT TT
2678	mH7	TTA AAC TGG GTT TTT CT
2679	mH8	GKG CTG YTC YTC TGC CT
2680	mH9	TTA AGT CTT CTG TAC CTG
2730	MH11	TCAGTAACTGCAGGTGTCCA
2731	MH12	TTTTAAAAGGTGTCCAGTGT
2732	MH13	GCAACAGCTACAGGTGTCCA
2733	MH14	CAGCTACAG RT GTCCACTCC
2734	MH15	ATTTCCAAGCTGTGTCCTGTCC
2735	MH16	CTCCTGTCAGGAACTGCAGGTGT
2736	MH17	CAGTGGTTACAGGGGTCAATTCA
2737	MH18	CTGTT SACAGCCH TTCC KGGT
2738	MH19	CTGATGGCAGCTGCCCAAAGT
2739	MH20	TTTATCAAGGTGTGCATTGT

C

2650 5' TCACTGGATGGTGGGAAGATGGATACA 3'
2656 5' GACATTTGGGAAGGACTGACTCTC 3'
2706 5' CAG GGG GCT CTC GCA GGA GAC GAG 3'

FIGURE 1

HuIV-26 VL

GACATTGTGATGACACAGTCTCCATCTTTGTTGAGTGTGTCAGCAGGAGAGAAGGTCACT
ATGAGCTGCAAGTCCAGTCAGAGTCTGTTAAACAGTGGAAATCAAAGAAGTACTTGGCC
TGGTACCAGCAGAAACCAGGGCAGCCTCCTAAACTGTTGATCTATGGGGCATCCACTAGG
GAATCTGGGGTCCCTGATCGCTTCACAGGCAGTGGATCTGGAACCGATTTCACTCTTATC
ATCAGCAGTGTGCAGGCTGAAGACCTGGCAGTTTATTACTGTCAGAATGATCATAGTTAT
CCGTACACGTTTCGGAGGGGGGACCAAGCTGGAAATAAAA

FIGURE 2A

HuIV-26 VH

GAGGTGAAGCTTCTCGAGTCTGGAGGTGGCCTGGTGCAGCCTGGAGGATCCCTGAAACT
CTCCTGTGCAGCCTCAGGATTCGATTTTAGTAGATACTGGATGAGTTGGGTCCGGCAGG
CTCCAGGGAAAGGGCTAGAATGGATTGGAGAAATTAATCCAGATAGCAGTACGATAAAC
TATACGCCATCTCTAAAGGATAAATTCATCATCTCCAGAGACAACGCCAAAAATACGCT
GTACCTGCAAATGAGCAAAGTGAGATCTGAGGACACAGCCCTTTATTACTGTGCAAGAC
CGGTTGATGGTTACTACGATGCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTC
TCCTCA

FIGURE 2B

Vk Domain

	10	20	30	40
HUIV26	1	DI VMTQSPSLLSV	A G E K V T M S C K S S Q S L L N S G N Q K N Y L A W Y Q Q K P G Q P P K L L I Y	
VKIV		DI VMTQSPD S L A V S L G E R A T I N C K S S Q S V L Y S S N N K N Y L A W Y Q Q K P G Q P P K L L I Y		
	50	60	70	80
HUIV26		G A S T R E S G V P D R F T G S G S G T D F T L I I S S V Q A E D L A V Y Y C Q N D H S Y P Y T F G G G T K L E I K		
VKIV/JK2		W A S T R E S G V P D R F S G S G S G T D F T L T I S S L Q A E D V A V Y Y C Q Q D H S Y P Y T F G Q G T K L E I K		

Vh Domain

	10	20	30	40
HUIV26	1	E V K L L E S G G L V Q P G G S L K L S C A A S G F D F S R Y W M S W V R Q A P G K G L E W I G		
VHIII		E V Q L V E S G G L V Q P G G S L R L S C A A S G F T F S S Y W M S W V R Q A P G K G L E W V A		
	50	60	70	80
HUIV26		E I N P D S S T I N Y T P S L K D K F I I S R D N A K N T L Y L Q M S K V R S E D T A L Y Y C A R		
VHIII		N I K Q D G S E K Y Y V D S V K G R F T I S R D N A K N S L Y L Q M N S L R A E D T A V Y Y C A R		
	abc	100	110	
HUIV26		P V D G Y Y D A M D Y W G Q G T S V T V S S		
JH6		P D Y Y Y Y G M D V W G Q G T T V T V S S		

FIGURE 2C

HUI77 VL sequence

GATGTTTTGATGACCCAACTCCACTCTCCCTGCCTGTCAGTCTTGGAGATCAAGCCTCC
ATCTCTTGCAGATCTAGTCAGAGCATTGTACATAGTAATGGAAACACCTATTTAGAATGG
TACCTGCAGAAACCAGGCCAGTCTCCAAAGCTCCTGATCTACAAAGTTTCCAACCGATTT
TCTGGTGTCCCAGACAGGTTTCAGTGGCAGTGGATCAGGGACAGATTTCACTCAAGATC
AGCAGAGTGGAGGCTGAGGATCTGGGAGTTTATTACTGCTTTCAAGGTTACATGTTCCG
TGGACGTTTCGGTGGAGGCACCAAGCTGGAAATCAAA

FIGURE 3A

HUI77 VH SEQUENCE

CAGGTTACTCTGAAAGAGACTGGCCCTGGGATATTGCAGCCCTCCCAGACCCTCAGTCTG
ACTTGTTCTTTCTCTGGGTTTTCACTGAGCACTTCTGGTATGGGTGTAGGCTGGATTTCGT
CAGCCTTCAGGAGAGGGTCTAGAGTGGCTGGCAGACATTTGGTGGGATGACAATAAGTAC
TATAACCCATCCCTGAAGAGCCGGCTCACAATCTCCAAGGATACCTCCAGCAACCAGGTA
TTCCTCAAGATCACCAGTGTGGACACTGCAGATACTGCCACTTACTACTGTGCTCGAAGA
GCTAACTATGGTAACCCCTACTATGCTATGGACTACTGGGGTCAAGGAACCTCAGTCACC
GTCTCCTCA

FIGURE 3B

Vk Domain

[illegible]

VH Domain

HUI-77	1	10	20	30	ab	40
	Q	V	T	L	K	E
	G	P	G	I	L	Q
	P	S	Q	T	L	S
	L	T	C	S	F	S
	G	F	S	L	S	T
	S	G	M	G	V	G
	I	R	Q	P	S	G
	E	G	L	E	W	L
	A					
VHII	Q	V	T	L	K	E
	S	G	P	A	L	V
	K	P	T	Q	T	L
	T	C	T	F	S	G
	F	S	L	S	T	S
	G	M	R	V	S	W
	I	R	Q	P	P	G
	K	A	L	E	W	L
	A					
HUI-77	50	60	70	80	abc	90
	D	I	W	D	D	N
	K	Y	N	P	S	L
	K	S	R	L	T	I
	S	K	D	T	S	S
	N	Q	V	F	L	K
	I	T	S	V	D	T
	A	T	Y	Y	C	A
	R	I	D	W	D	D
	K	F	Y	S	T	S
	L	K	T	R	L	T
	I	S	K	D	T	S
	K	N	Q	V	V	L
	T	M	D	P	V	D
	T	A	T	Y	Y	C
	A					
HUI-77	100	cde	110			
	R	A	N	Y	G	N
	P	Y	A	M	D	Y
	W	G	Q	T	S	V
	T	V	T	V	S	S
	R	A	N	Y	Y	Y
	A	M	D	V	W	G
	Q	T	T	V	T	V
	S	S				
JH6						

FIGURE 3C

HUI77 VL sequence

HUI77 VL	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15
DPK13	GAT	GTT	TTG	ATG	ACC	CAA	ACT	CCA	CTC	TCC	CTG	CCT	GTC	AGT	CTT
	---	A--	G--	---	---	--G	---	---	---	---	---	--C	---	-CC	-C-
	CDR1														
HUI77 VL	16	17	18	19	20	21	22	23	24	25	26	27	27a	27b	27c
DPK13	GGA	GAT	CAA	GCC	TCC	ATC	TCT	TGC	AGA	TCT	AGT	CAG	AGC	ATT	GTA
	---	--G	-CG	---	---	---	--C	---	--G	---	---	---	---	C-C	T-G
	27d	27e	27f	28	29	30	31	32	33	34	35	36	37	38	39
HUI77 VL	CAT	AGT	...	AAT	GGA	AAC	ACC	TAT	TTA	GAA	TGG	TAC	CTG	CAG	AAA
DPK13	G--	---	GAT	G--	---	---	---	---	--G	--C	---	---	---	---	--G
	CDR2														
HUI77 VL	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54
DPK13	CCA	GGC	CAG	TCT	CCA	AAG	CTC	CTG	ATC	TAC	AAA	GTT	TCC	AAC	CGA
	---	--G	---	---	---	C--	---	---	---	--T	-CG	C--	---	T-T	--G
	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69
HUI77 VL	TTT	TCT	GGT	GTC	CCA	GAC	AGG	TTC	AGT	GGC	AGT	GGA	TCA	GGG	ACA
DPK13	GCC	---	--A	---	---	---	---	---	---	---	---	--G	---	--C	--T
	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84
HUI77 VL	GAT	TTC	ACA	CTC	AAG	ATC	AGC	AGA	GTG	GAG	GCT	GAG	GAT	CTG	GGA
DPK13	---	---	---	--G	--A	---	---	--G	---	---	---	---	---	G-T	---
	CDR3														
HUI77 VL	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99
DPK13	GTT	TAT	TAC	TGC	TTT	CAA	GGT	TCA	CAT	GTT	CCG	TGG	ACG	TTC	GGT
	---	---	---	---	A-G	---	---	---	---	---	---	---	---	---	--C
HUI77 VL	100	101	102	103	104	105	106	107							
DPK13	GGA	GGC	ACC	AAG	CTG	GAA	ATC	AAA							
JK1	CA-	--G	---	---	G--	---	---	---							

FIGURE 3D

HUIV26 LCDR3

IV26-17.1 CTT GGT CCC CTG GCC AAA AGT GTA CGG ATA ACT ATG ATC ATT MNN ACA GTA ATA AAC TGC CAC ATC
IV26-17.2 CTT GGT CCC CTG GCC AAA AGT GTA CGG ATA ACT ATG ATC MNN CTG ACA GTA ATA AAC TGC CAC ATC
IV26-17.3 CTT GGT CCC CTG GCC AAA AGT GTA CGG ATA ACT ATG MNN ATT CTG ACA GTA ATA AAC TGC CAC ATC
IV26-17.4 CTT GGT CCC CTG GCC AAA AGT GTA CGG ATA ACT MNN ATC ATT CTG ACA GTA ATA AAC TGC CAC ATC
IV26-17.5 CTT GGT CCC CTG GCC AAA AGT GTA CGG ATA MNN ATG ATC ATT CTG ACA GTA ATA AAC TGC CAC ATC
IV26-17.6 CTT GGT CCC CTG GCC AAA AGT GTA CGG MNN ACT ATG ATC ATT CTG ACA GTA ATA AAC TGC CAC ATC
IV26-17.7 CTT GGT CCC CTG GCC AAA AGT GTA MNN ATA ACT ATG ATC ATT CTG ACA GTA ATA AAC TGC CAC ATC
IV26-17.8 CTT GGT CCC CTG GCC AAA AGT MNN CGG ATA ACT ATG ATC ATT CTG ACA GTA ATA AAC TGC CAC ATC
IV26-17.9 CTT GGT CCC CTG GCC AAA MNN GTA CGG ATA ACT ATG ATC ATT CTG ACA GTA ATA AAC TGC CAC ATC

HUIV26 HCDR3

IV26-h7.1 CGT GGT TCC TTG CCC CCA GTA GTC CAT AGC ATC GTA GTA ACC ATC AAC MNN TCT CGC ACA GTA ATA CAC
IV26-h7.2 CGT GGT TCC TTG CCC CCA GTA GTC CAT AGC ATC GTA GTA ACC ATC MNN CGG TCT CGC ACA GTA ATA CAC
IV26-h7.3 CGT GGT TCC TTG CCC CCA GTA GTC CAT AGC ATC GTA GTA ACC MNN AAC CGG TCT CGC ACA GTA ATA CAC
IV26-h7.4 CGT GGT TCC TTG CCC CCA GTA GTC CAT AGC ATC GTA MNN ATC AAC CGG TCT CGC ACA GTA ATA CAC
IV26-h7.5 CGT GGT TCC TTG CCC CCA GTA GTC CAT AGC ATC GTA MNN ACC ATC AAC CGG TCT CGC ACA GTA ATA CAC
IV26-h7.6 CGT GGT TCC TTG CCC CCA GTA GTC CAT AGC ATC MNN GTA ACC ATC AAC CGG TCT CGC ACA GTA ATA CAC
IV26-h7.7 CGT GGT TCC TTG CCC CCA GTA GTC CAT MNN ATC GTA GTA ACC ATC AAC CGG TCT CGC ACA GTA ATA CAC
IV26-h7.8 CGT GGT TCC TTG CCC CCA GTA GTC CAT MNN ATC GTA GTA ACC ATC AAC CGG TCT CGC ACA GTA ATA CAC
IV26-h7.9 CGT GGT TCC TTG CCC CCA GTA GTC MNN AGC ATC GTA GTA ACC ATC AAC CGG TCT CGC ACA GTA ATA CAC
IV26-h7.10 CGT GGT TCC TTG CCC CCA GTA MNN CAT AGC ATC GTA GTA ACC ATC AAC CGG TCT CGC ACA GTA ATA CAC
IV26-h7.11 CGT GGT TCC TTG CCC CCA MNN GTC CAT AGC ATC GTA GTA ACC ATC AAC CGG TCT CGC ACA GTA ATA CAC

FIGURE 4A

HUIV26 LCDR1a

IV26L1-1 GTTCTTTTGGTTTCCGCWGTTTAACAGACTCTGGCTGGAMNNGCAGTTGATGGTGGCCCT
IV26L1-2 GTTCTTTTGGTTTCCGCWGTTTAACAGACTCTGGCTMNNTTGCAGTTGATGGTGGCCCT
IV26L1-3 GTTCTTTTGGTTTCCGCWGTTTAACAGACTCTGMNNGGACTTGCAGTTGATGGTGGCCCT
IV26L1-4 GTTCTTTTGGTTTCCGCWGTTTAACAGACTMNNGCTGGACTTGCAGTTGATGGTGGCCCT
IV26L1-5 GTTCTTTTGGTTTCCGCWGTTTAACAGMNNTGGCTGGACTTGCAGTTGATGGTGGCCCT
IV26L1-6 GTTCTTTTGGTTTCCGCWGTTTAAMNNACTCTGGCTGGACTTGCAGTTGATGGTGGCCCT
IV26L1-7 GTTCTTTTGGTTTCCGCWGTTMNNCAGACTCTGGCTGGACTTGCAGTTGATGGTGGCCCT
IV26L1-8 GTTCTTTTGGTTTCCGCWMNNTAACAGACTCTGGCTGGACTTGCAGTTGATGGTGGCCCT

HUIV26 LCDR1b

IV26L1-9 TGGTTTCTGCTGGTACCAAGCTAAGTAGTTCTTTTGGTTTCCMNNGTTTAAACAGACTCTGGCT
IV26L1-10 TGGTTTCTGCTGGTACCAAGCTAAGTAGTTCTTTTGGTTMNNGCWGTTTAAACAGACTCTGGCT
IV26L1-11 TGGTTTCTGCTGGTACCAAGCTAAGTAGTTCTTTTGMNNTCCGCWGTTTAAACAGACTCTGGCT
IV26L1-12 TGGTTTCTGCTGGTACCAAGCTAAGTAGTTCTTMNNGTTTCCGCWGTTTAAACAGACTCTGGCT
IV26L1-13 TGGTTTCTGCTGGTACCAAGCTAAGTAGTTMNNTTGGTTTCCGCWGTTTAAACAGACTCTGGCT
IV26L1-14 TGGTTTCTGCTGGTACCAAGCTAAGTAMNNTCTTTTGGTTTCCGCWGTTTAAACAGACTCTGGCT
IV26L1-15 TGGTTTCTGCTGGTACCAAGCTAAMNNGTTCTTTTGGTTTCCGCWGTTTAAACAGACTCTGGCT
IV26L1-16 TGGTTTCTGCTGGTACCAAGCMNNGTAGTTCTTTTGGTTTCCGCWGTTTAAACAGACTCTGGCT
IV26L1-17 TGGTTTCTGCTGGTACCAMNNTAAGTAGTTCTTTTGGTTTCCGCWGTTTAAACAGACTCTGGCT

HUIV26 LCDR2

IV26L2-1 GAATCGGTCAGGGACCCCGGATTCCCTGGTAGATGCMNNGTAAATGAGCAGCTTAGG
IV26L2-2 GAATCGGTCAGGGACCCCGGATTCCCTGGTAGAMNCCCGTAAATGAGCAGCTTAGG
IV26L2-3 GAATCGGTCAGGGACCCCGGATTCCCTGGTMNNTGCCCGTAAATGAGCAGCTTAGG
IV26L2-4 GAATCGGTCAGGGACCCCGGATTCCCTMNAGATGCCCGTAAATGAGCAGCTTAGG
IV26L2-5 GAATCGGTCAGGGACCCCGGATTCCMNNGTAGATGCCCGTAAATGAGCAGCTTAGG
IV26L2-6 GAATCGGTCAGGGACCCCGGAMNNTCTGGTAGATGCCCGTAAATGAGCAGCTTAGG
IV26L2-7 GAATCGGTCAGGGACCCCMNNTTCCCTGGTAGATGCCCGTAAATGAGCAGCTTAGG

HUIV26 HCDR1

IV26H1-1 TGGAGCCTGGCGGACCCAGCTCATCCAATAMNNACTAAAGGTGAATCCAGA
IV26H1-2 TGGAGCCTGGCGGACCCAGCTCATCCAMNNTCTACTAAAGGTGAATCCAGA
IV26H1-3 TGGAGCCTGGCGGACCCAGCTCATMNNTATCTACTAAAGGTGAATCCAGA
IV26H1-4 TGGAGCCTGGCGGACCCAGCTMNNTCAATATCTACTAAAGGTGAATCCAGA
IV26H1-5 TGGAGCCTGGCGGACCCAMNNTATCCAATATCTACTAAAGGTGAATCCAGA

HUIV26 HCDR2a

IV26H2-1 TAGAGATGGCGTATAGTTTATCGTACTGCTATCTGGATTATMNNGCCAAAYCCACTCCAGCCCTTTC
IV26H2-2 TAGAGATGGCGTATAGTTTATCGTACTGCTATCTGGATTMNNTTCGCCAAYCCACTCCAGCCCTTTC
IV26H2-3 TAGAGATGGCGTATAGTTTATCGTACTGCTATCTGMNNTATTTTCGCCAAYCCACTCCAGCCCTTTC
IV26H2-4 TAGAGATGGCGTATAGTTTATCGTACTGCTATCMNNTATTTATTCGCCAAYCCACTCCAGCCCTTTC
IV26H2-5 TAGAGATGGCGTATAGTTTATCGTACTGCTMNNTGGATTATTTTCGCCAAYCCACTCCAGCCCTTTC
IV26H2-6 TAGAGATGGCGTATAGTTTATCGTACTMNNTCTGGATTATTTTCGCCAAYCCACTCCAGCCCTTTC
IV26H2-7 TAGAGATGGCGTATAGTTTATCGTMNNGCTATCTGGATTATTTTCGCCAAYCCACTCCAGCCCTTTC
IV26H2-8 TAGAGATGGCGTATAGTTTATMNNACTGCTATCTGGATTATTTTCGCCAAYCCACTCCAGCCCTTTC
IV26H2-9 TAGAGATGGCGTATAGTTMNNTCTGCTATCTGGATTATTTTCGCCAAYCCACTCCAGCCCTTTC

HUIV26 HCDR2b

IV26H2-10 CGTTGTCTCTGGAGATGRTGAATYTATCCTTTAGAGATGGCGTATAMNNTATCGTACTGCTATCTGG
IV26H2-11 CGTTGTCTCTGGAGATGRTGAATYTATCCTTTAGAGATGGCGTMNNGTTTATCGTACTGCTATCTGG
IV26H2-12 CGTTGTCTCTGGAGATGRTGAATYTATCCTTTAGAGATGMNNTATAGTTTATCGTACTGCTATCTGG
IV26H2-13 CGTTGTCTCTGGAGATGRTGAATYTATCCTTTAGAGAMNNTATAGTTTATCGTACTGCTATCTGG
IV26H2-14 CGTTGTCTCTGGAGATGRTGAATYTATCCTTTAGMNNTGGCGTATAGTTTATCGTACTGCTATCTGG
IV26H2-15 CGTTGTCTCTGGAGATGRTGAATYTATCCTTMNNAAGATGGCGTATAGTTTATCGTACTGCTATCTGG
IV26H2-16 CGTTGTCTCTGGAGATGRTGAATYTATCMNNTAGAGATGGCGTATAGTTTATCGTACTGCTATCTGG
IV26H2-17 CGTTGTCTCTGGAGATGRTGAATYTAMNNTTTAGAGATGGCGTATAGTTTATCGTACTGCTATCTGG

FIGURE 4B

Beneficial Mutations for HuIV-26 Antibody

CDRs	H1			H2				H3			L1					L2	L3	
Kabat Number	31	34	35	57	62	64	65	97	98	102	27	27d	27e	27f	29		93	94
HuIV-26	R	M	S	I	S	K	D	D	G	Y	Q	N	S	G	Q		S	Y
Mutations	H	I	T	A	Y	Q	S	P	P	P	R	S	Y	Y	K		Q	N
			A	S	A			G	A	N	S		W	R			G	S
			G		H			T	H				H	H			L	P
				G				A					R	I			A	M
																	T	
																	V	/

FIGURE 4C

HUI77 LCDR3

I77-I7.1 CTT GGT GCC CTG GCC GAA CGT CCA CGG AAC ATG TGA ACC TTG MNN GCA GTA ATA AAC TCC AAC ATC
I77-I7.2 CTT GGT GCC CTG GCC GAA CGT CCA CGG AAC ATG TGA ACC MNN AAA GCA GTA ATA AAC TCC AAC ATC
I77-I7.3 CTT GGT GCC CTG GCC GAA CGT CCA CGG AAC ATG TGA MNN TTG AAA GCA GTA ATA AAC TCC AAC ATC
I77-I7.4 CTT GGT GCC CTG GCC GAA CGT CCA CGG AAC ATG MNN ACC TTG AAA GCA GTA ATA AAC TCC AAC ATC
I77-I7.5 CTT GGT GCC CTG GCC GAA CGT CCA CGG AAC MNN TGA ACC TTG AAA GCA GTA ATA AAC TCC AAC ATC
I77-I7.6 CTT GGT GCC CTG GCC GAA CGT CCA CGG MNN ATG TGA ACC TTG AAA GCA GTA ATA AAC TCC AAC ATC
I77-I7.7 CTT GGT GCC CTG GCC GAA CGT CCA MNN AAC ATG TGA ACC TTG AAA GCA GTA ATA AAC TCC AAC ATC
I77-I7.8 CTT GGT GCC CTG GCC GAA CGT MNN CGG AAC ATG TGA ACC TTG AAA GCA GTA ATA AAC TCC AAC ATC
I77-I7.9 CTT GGT GCC CTG GCC GAA MNN CCA CGG AAC ATG TGA ACC TTG AAA GCA GTA ATA AAC TCC AAC ATC

HUI77 HCDR3

I77-h7.1 CGT GGT TCC TTG CCC CCA GTA GTC CAT AGC ATA GTA GGG GTT ACC ATA GTT AGC MNN TCG AGC ACA GTA ATA CGT
I77-h7.2 CGT GGT TCC TTG CCC CCA GTA GTC CAT AGC ATA GTA GGG GTT ACC ATA GTT MNN TCT TCG AGC ACA GTA ATA CGT
I77-h7.3 CGT GGT TCC TTG CCC CCA GTA GTC CAT AGC ATA GTA GGG GTT ACC ATA MNN AGC TCT TCG AGC ACA GTA ATA CGT
I77-h7.4 CGT GGT TCC TTG CCC CCA GTA GTC CAT AGC ATA GTA GGG GTT ACC MNN GTT AGC TCT TCG AGC ACA GTA ATA CGT
I77-h7.5 CGT GGT TCC TTG CCC CCA GTA GTC CAT AGC ATA GTA GGG MNN ACC ATA GTT AGC TCT TCG AGC ACA GTA ATA CGT
I77-h7.6 CGT GGT TCC TTG CCC CCA GTA GTC CAT AGC ATA GTA GGG MNN ACC ATA GTT AGC TCT TCG AGC ACA GTA ATA CGT
I77-h7.7 CGT GGT TCC TTG CCC CCA GTA GTC CAT AGC ATA GTA MNN GTT ACC ATA GTT AGC TCT TCG AGC ACA GTA ATA CGT
I77-h7.8 CGT GGT TCC TTG CCC CCA GTA GTC CAT AGC ATA MNN GGG GTT ACC ATA GTT AGC TCT TCG AGC ACA GTA ATA CGT
I77-h7.9 CGT GGT TCC TTG CCC CCA GTA GTC CAT AGC MNN GTA GGG GTT ACC ATA GTT AGC TCT TCG AGC ACA GTA ATA CGT
I77-h7.10 CGT GGT TCC TTG CCC CCA GTA GTC CAT MNN ATA GTA GGG GTT ACC ATA GTT AGC TCT TCG AGC ACA GTA ATA CGT
I77-h7.11 CGT GGT TCC TTG CCC CCA GTA GTC MNN AGC ATA GTA GGG GTT ACC ATA GTT AGC TCT TCG AGC ACA GTA ATA CGT
I77-h7.12 CGT GGT TCC TTG CCC CCA GTA MNN CAT AGC ATA GTA GGG GTT ACC ATA GTT AGC TCT TCG AGC ACA GTA ATA CGT
I77-h7.13 CGT GGT TCC TTG CCC CCA MNN GTC CAT AGC ATA GTA GGG GTT ACC ATA GTT AGC TCT TCG AGC ACA GTA ATA CGT

FIGURE 5A

HUI77 LCDR1a

3000 ATA GGT GTT TCC ATT ACT ATG TAC AAT GCT CTG ACT AGA MNN GCA GGA GAT GGA GGC C
3001 ATA GGT GTT TCC ATT ACT ATG TAC AAT GCT CTG ACT MNN CCT GCA GGA GAT GGA GGC C
3002 ATA GGT GTT TCC ATT ACT ATG TAC AAT GCT CTG MNN AGA CCT GCA GGA GAT GGA GGC C
3003 ATA GGT GTT TCC ATT ACT ATG TAC AAT GCT MNN ACT AGA CCT GCA GGA GAT GGA GGC C
3004 ATA GGT GTT TCC ATT ACT ATG TAC AAT MNN CTG ACT AGA CCT GCA GGA GAT GGA GGC C
3005 ATA GGT GTT TCC ATT ACT ATG TAC MNN GCT CTG ACT AGA CCT GCA GGA GAT GGA GGC C
3006 ATA GGT GTT TCC ATT ACT ATG MNN AAT GCT CTG ACT AGA CCT GCA GGA GAT GGA GGC C
3007 ATA GGT GTT TCC ATT ACT MNN TAC AAT GCT CTG ACT AGA CCT GCA GGA GAT GGA GGC C

HUI77 LCDR1b

3008 TGG CTT CTG CAG GTA CCA TTC CAA ATA GGT GTT TCC ATT MNN ATG TAC AAT GCT CTG ACT
3009 TGG CTT CTG CAG GTA CCA TTC CAA ATA GGT GTT TCC MNN ACT ATG TAC AAT GCT CTG ACT
3010 TGG CTT CTG CAG GTA CCA TTC CAA ATA GGT GTT MNN ATT ACT ATG TAC AAT GCT CTG ACT
3011 TGG CTT CTG CAG GTA CCA TTC CAA ATA GGT MNN TCC ATT ACT ATG TAC AAT GCT CTG ACT
3012 TGG CTT CTG CAG GTA CCA TTC CAA ATA MNN GTT TCC ATT ACT ATG TAC AAT GCT CTG ACT
3013 TGG CTT CTG CAG GTA CCA TTC CAA MNN GGT GTT TCC ATT ACT ATG TAC AAT GCT CTG ACT
3014 TGG CTT CTG CAG GTA CCA TTC MNN ATA GGT GTT TCC ATT ACT ATG TAC AAT GCT CTG ACT
3015 TGG CTT CTG CAG GTA CCA MNN CAA ATA GGT GTT TCC ATT ACT ATG TAC AAT GCT CTG ACT

HUI77 LCDR2

3016 GAA CCT GTC TGG GAC TCC AGA AAA CCG GTT GGA AAC MNN ATA GAT CAG GAG CTG TGG
3017 GAA CCT GTC TGG GAC TCC AGA AAA CCG GTT GGA MNN TTT ATA GAT CAG GAG CTG TGG
3018 GAA CCT GTC TGG GAC TCC AGA AAA CCG GTT MNN AAC TTT ATA GAT CAG GAG CTG TGG
3019 GAA CCT GTC TGG GAC TCC AGA AAA CCG MNN GGA AAC TTT ATA GAT CAG GAG CTG TGG
3020 GAA CCT GTC TGG GAC TCC AGA AAA MNN GTT GGA AAC TTT ATA GAT CAG GAG CTG TGG
3021 GAA CCT GTC TGG GAC TCC AGA MNN CCG GTT GGA AAC TTT ATA GAT CAG GAG CTG TGG
3022 GAA CCT GTC TGG GAC TCC MNN AAA CCG GTT GGA AAC TTT ATA GAT CAG GAG CTG TGG

HUI77 HCDR1

3023 TGG GGG CTG ACG GAT CCA GCC CAC ACC CAT TCC AGA MNN GCT GAG TGA GAA CCC AGA
3024 TGG GGG CTG ACG GAT CCA GCC CAC ACC CAT TCC MNN AGT GCT GAG TGA GAA CCC AGA
3025 TGG GGG CTG ACG GAT CCA GCC CAC ACC CAT MNN AGA AGT GCT GAG TGA GAA CCC AGA
3026 TGG GGG CTG ACG GAT CCA GCC CAC ACC MNN TCC AGA AGT GCT GAG TGA GAA CCC AGA
3027 TGG GGG CTG ACG GAT CCA GCC CAC MNN CAT TCC AGA AGT GCT GAG TGA GAA CCC AGA
3028 TGG GGG CTG ACG GAT CCA GCC MNN ACC CAT TCC AGA AGT GCT GAG TGA GAA CCC AGA
3029 TGG GGG CTG ACG GAT CCA MNN CAC ACC CAT TCC AGA AGT GCT GAG TGA GAA CCC AGA

HUI77 HCDR2a

3038 CAG AGA TGG GTT GTA GTA TTT ATT GTC ATC CCA CCA AAT MNN TGC AAG CCA CTC CAG GGC
3039 CAG AGA TGG GTT GTA GTA TTT ATT GTC ATC CCA CCA MNN GTC TGC AAG CCA CTC CAG GGC
3040 CAG AGA TGG GTT GTA GTA TTT ATT GTC ATC CCA MNN AAT GTC TGC AAG CCA CTC CAG GGC
3041 CAG AGA TGG GTT GTA GTA TTT ATT GTC ATC MNN CCA AAT GTC TGC AAG CCA CTC CAG GGC
3042 CAG AGA TGG GTT GTA GTA TTT ATT GTC MNN CCA CCA AAT GTC TGC AAG CCA CTC CAG GGC
3043 CAG AGA TGG GTT GTA GTA TTT ATT MNN ATC CCA CCA AAT GTC TGC AAG CCA CTC CAG GGC
3044 CAG AGA TGG GTT GTA GTA TTT MNN GTC ATC CCA CCA AAT GTC TGC AAG CCA CTC CAG GGC
3045 CAG AGA TGG GTT GTA GTA MNN ATT GTC ATC CCA CCA AAT GTC TGC AAG CCA CTC CAG GGC

HUI77 HCDR2b

3030 CTT GGA GAT GGT GAG CCT GCT CTT CAG AGA TGG GTT GTA MNN TTT ATT GTC ATC CCA CCA
3031 CTT GGA GAT GGT GAG CCT GCT CTT CAG AGA TGG GTT MNN GTA TTT ATT GTC ATC CCA CCA
3032 CTT GGA GAT GGT GAG CCT GCT CTT CAG AGA TGG MNN GTA GTA TTT ATT GTC ATC CCA CCA
3033 CTT GGA GAT GGT GAG CCT GCT CTT CAG AGA MNN GTT GTA GTA TTT ATT GTC ATC CCA CCA
3034 CTT GGA GAT GGT GAG CCT GCT CTT CAG MNN TGG GTT GTA GTA TTT ATT GTC ATC CCA CCA
3035 CTT GGA GAT GGT GAG CCT GCT CTT MNN AGA TGG GTT GTA GTA TTT ATT GTC ATC CCA CCA
3036 CTT GGA GAT GGT GAG CCT GCT MNN CAG AGA TGG GTT GTA GTA TTT ATT GTC ATC CCA CCA
3037 CTT GGA GAT GGT GAG CCT MNN CTT CAG AGA TGG GTT GTA GTA TTT ATT GTC ATC CCA CCA

FIGURE 5B

Beneficial Mutations for H_uL-77 Antibody

CDRs	H1	H2	H3	L1	L2	L3
Kabat Number	32 35b	59 64	95 100 100e 102	27c 27d 27e 28 30 33	50 51 53 54 56	89 90 91 92 93 94 97
HuL-77	S G	Y K	R N M Y	V H S N N L	K V N R S	F Q G S H V T
Mutations	P W W L A	S P A P	P V Q K Q W N T L T M H V	P L W Y Y F W S W V	S A S L W F	V R S W L T A H W E T S H K I

FIGURE 5C

Beneficial mutations chosen for combinatorial library

CDRs	H1	H2	H3	L1	L3	SPEkon	SPEkoff
Kabat Number	35	57 62	102	27d 27e 27f	93	O.D.560	O.D.560
wild type	S	I S	Y	N S G	S		
HuIV-26	S	I S	Y	N S G	S		
Mutations	T A	A Y A H	P	S Y Y W R H H R	Q		

Beneficial mutants

4.1-2D4	S	I S	P	N S G	Q		
L1b-F11	S	I S	P	N S Y	Q	0.745	0.483
H2a-G8	S	A S	P	N S G	Q	0.397	0.159
2D4H1-C3	A	I S	P	N S G	Q		
DcomA4	S	A Y	P	N Y Y	Q	0.981	0.769
DcomB1	A	A Y	P	N Y H	Q	1.018	0.714
DcomE1						1.031	0.758
DcomH2						1.07	0.705
DcomD2	S	A S	P	N R Y	Q	1.104	0.729
DcomD3	T	A Y	P	N S Y	Q	1.035	0.736
DcomD6	S	A Y	P	N W Y	Q	1.102	0.753
DcomA11						1.003	0.786
DcomE3	T	A Y	P	N R Y	Q	0.991	0.754
DcomG2	A	A Y	P	N R Y	Q	1.161	0.856
DcomA7	T	V S	P	N Y Y	Q	0.986	0.77
DcomB8	T	A A	P	N W Y	Q	0.998	0.807
DcomA2						1.026	0.74
DcomB10	T	A H	P	N W Y	Q	0.87	0.735
DcomC8	S	A A	P	N W Y	Q	0.978	0.763
DcomD7	T	A Y	P	N W Y	Q	1.083	0.794
DhuG5							
DhuH8							
DcomD11	A	A A	P	N W H	Q	1.125	0.752
DcomE11	A	A H	P	N W H	Q	0.973	0.732

Primers for combinatorial mutation

dH5762 TCTCTGGAGATGGTGAATTTACGTAAGTCTATCTGGATT
dL27def CTAAGTAGTTCTTTTGGTTGTTATAACAGACTCTGGCTGGA
H1-35 TGGAGCCTGGCGGACCCAGGHCATCCAATATCTACTAAAGGTGAATCCAGA
H2-5762a TCTCTGGAGATGGTGAATCTATCCTTTAGGGM TGGCGTATAGTTGGCCGTAAGTCTATCTGGATT
H2-5762b TCTCTGGAGATGGTGAATCTATCCTTTAGGTR TGGCGTATAGTTGGCCGTAAGTCTATCTGGATT
L1-27def1 CTAAGTAGTTCTTTTGGTTGTRGTRGYTTAACAGACTCTGGCTGGA
L1-27def2 CTAAGTAGTTCTTTTGGTTGCSGTRGYTTAACAGACTCTGGCTGGA
L1-27def3 CTAAGTAGTTCTTTTGGTTGTRGCKGYTTAACAGACTCTGGCTGGA
L1-27def4 CTAAGTAGTTCTTTTGGTTGCSGCKGYTTAACAGACTCTGGCTGGA
L1-27def5 CTAAGTAGTTCTTTTGGTTGTRCCAGYTTAACAGACTCTGGCTGGA
L1-27def6 CTAAGTAGTTCTTTTGGTTGCSCCAGYTTAACAGACTCTGGCTGGA

FIGURE 6

Beneficial mutations chosen for combinatorial library

CDRs	H1	H2	H3	L1	L3	Screen	Screen
Kabat Number	32 35b	59	100e	27d 28 33	91 94	kon	koff
wild type	S G	Y	M	H N L	G V		
Hu1-77	S G	Y	M	H N L	V		
Mutations	P W L A	S A P	Q	L Y F S W	S		

Beneficial combinatorial mutants

Qh2b-B7	S G	A	Q	H N L	S		
QH2b-A3	S G	S	Q	H N L			
Qcom1B6	P W	S	Q	S W L	S	1.319	0.534
Qcom1B8	P W	S	Q	S Y L	S	1.266	0.497
Qcom1E7						1.247	0.46
Qcom1G10						1.282	0.452
Qcom2G2						1.304	0.402
Qcom1C3	P W	A	Q	S W L	S	1.342	0.535
Qcom2A2						1.605	0.647
Qcom1G3						1.274	0.464
Qcom1D3	P W	T	Q	S W L	S	1.647	0.984
QhuD9							
QhuD93							
Qcom1E3	P W	A	Q	S Q L	S	1.225	0.347
Qcom2F6						1.311	0.321
Qcom1H6	P W	S	Q	S Q L	S	1.295	0.323
Qcom1H7	P W	A	Q	H Q F	S F	1.634	1.08
Qcom2A4	P A	A	Q	S Y L	S	1.304	0.265
Qcom2B11	P W	A	Q	H Y L	S	1.11	0.221
Qcom2C1	P W	Y	Q	S W F	S	1.189	0.213
Qcom2D9	P W	S	Q	H W L	S	1.101	0.209
Qcom2E3	P W	A	Q	H W L	S	1.117	0.248

Primers for combinatorial mutation

dL27d-33 CTT CTG CAG GTA CCA TTC GTIA TAC AAT GCT CTG ACT AGA

H1-35b1 TGG GGG CTG ACG GAT CCA CMA CAC ACC CAT TCC AGR AGT GCT GAG TGA GAA CCC AGA

H1-35b2 TGG GGG CTG ACG GAT CCA GSC CAC ACC CAT TCC AGR AGT GCT GAG TGA GAA CCC AGA

H2-59 GCT CTT CAG AGA TGG GTT AGV GTA TTT ATT GTC ATC CCA C

L27d1 CTT CTG CAG GTA CCA TTC MAA ATA GGT GTT TCC CCA ACT CRA TAC AAT GCT CTG ACT AGA

L27d2 CTT CTG CAG GTA CCA TTC MAA ATA GGT GTT TCC GTA ACT CRA TAC AAT GCT CTG ACT AGA

L27d3 CTT CTG CAG GTA CCA TTC MAA ATA GGT GTT TCC CTG ACT CRA TAC AAT GCT CTG ACT AGA

L27d4 CTT CTG CAG GTA CCA TTC MAA ATA GGT GTT TCC CCA ACT GTG TAC AAT GCT CTG ACT AGA

L27d5 CTT CTG CAG GTA CCA TTC MAA ATA GGT GTT TCC GTA ACT GTG TAC AAT GCT CTG ACT AGA

L27d6 CTT CTG CAG GTA CCA TTC MAA ATA GGT GTT TCC CTG ACT GTG TAC AAT GCT CTG ACT AGA

FIGURE 7

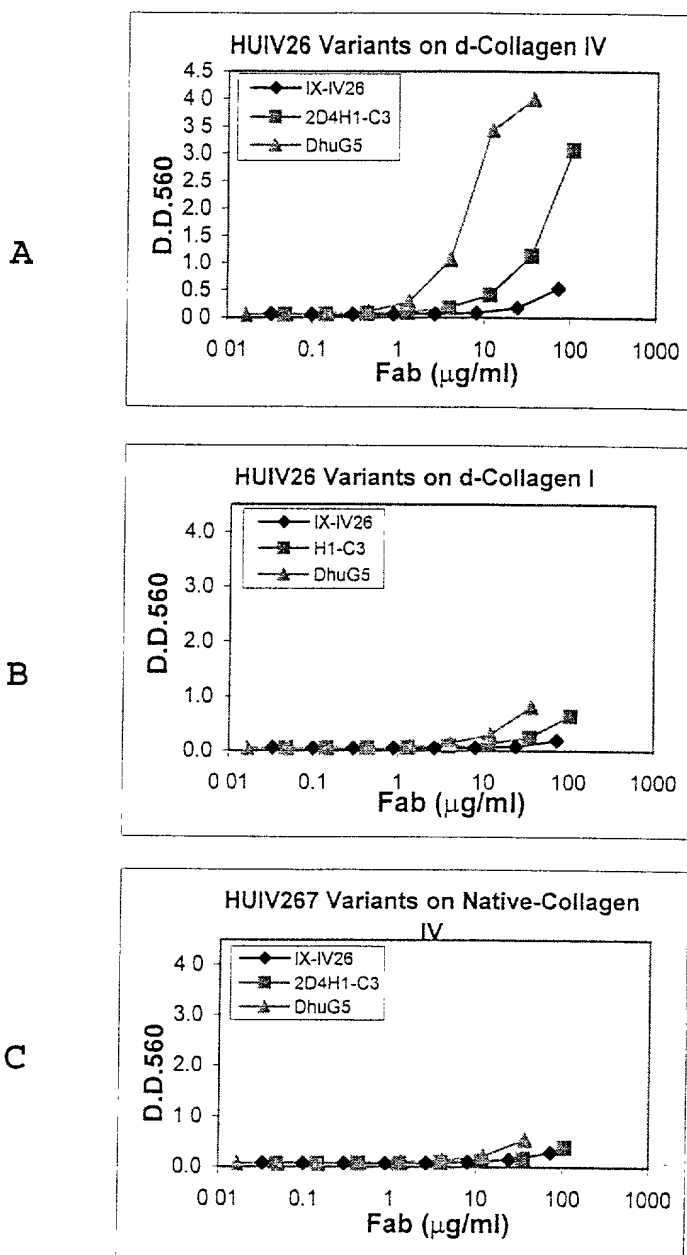
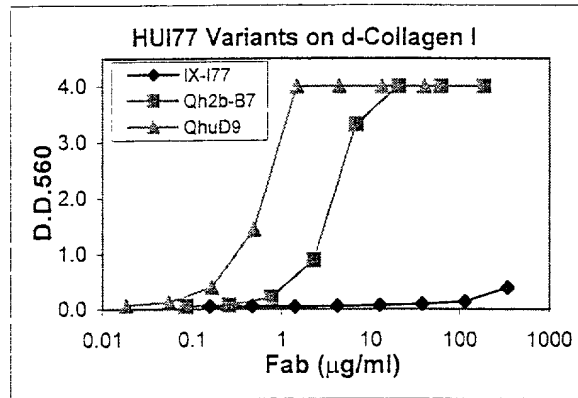
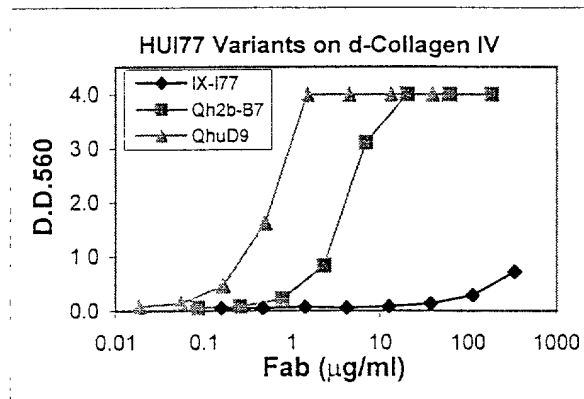


FIGURE 8

A



B



C

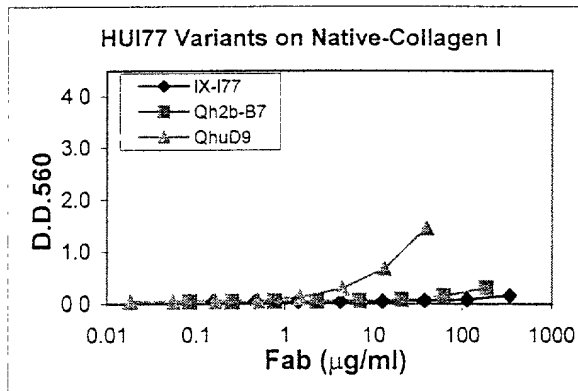


FIGURE 9

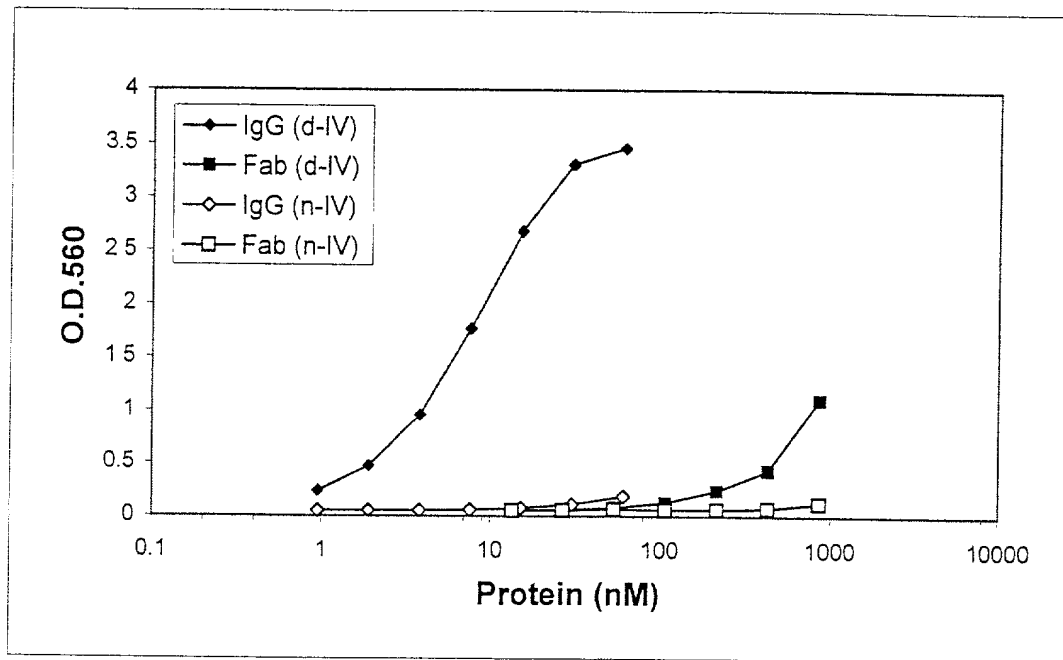


FIGURE 10

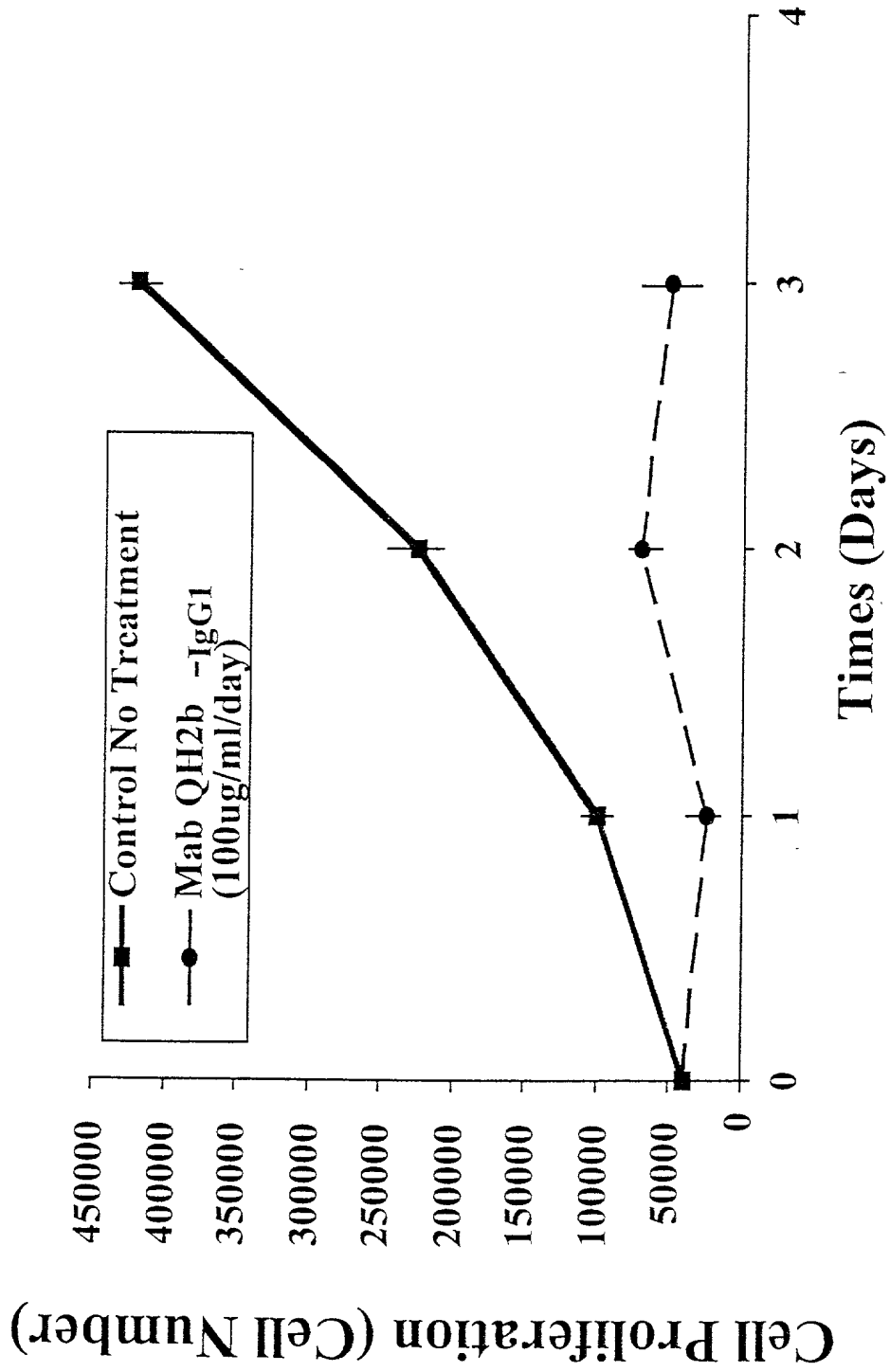


FIGURE 11